

SEQUENCE LISTING

<110> Gray, Kevin A.
Aboushadi, Nahla M.
Garrett, James B.

<120> Amylases, Nucleic Acids Encoding them and Methods For Making and Using them

<130> 09010-091WO1

<140> not assigned

<141> 2003-10-15

<150> US 60/423,626

<151> 2002-10-31

<160> 16

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1854

<212> DNA

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 35 40 45
 Lys Lys Val Ala Ser Leu Asp Glu Asp Trp Glu Thr Thr Val Leu Tyr
 50 55 60
 Ile Asp Glu Ala Asn Met Val Glu Ile Arg Ser Asp Val Lys Glu Leu
 65 70 75 80
 Gly Leu Ser Leu Leu Ser Tyr Asn Phe Leu Asp Ser Asp Asp Pro Ile
 85 90 95
 Tyr Met Ser Ile Val Lys Ile Ala Asn Asn Glu Asn Asn Ser Arg Asn
 100 105 110
 Ile Lys Val Phe Phe Ile His Asp Ile Asn Leu Tyr Ser Asn Pro Phe
 115 120 125
 Gly Asp Thr Ala Phe Tyr Asp Pro Leu Pro Leu Ser Ile Ile His Tyr
 130 135 140
 Lys Ser Lys Arg Tyr Leu Ala Phe Lys Val Phe Thr Thr Val Ser Thr
 145 150 155 160
 Leu Ser Glu Tyr Asn Ile Gly Lys Gly Asp Leu Ile Gly Asp Ile Tyr
 165 170 175
 Asp Gly Asn Leu Gly Leu Asn Gly Ile Glu Asn Gly Asp Val Asn Ser
 180 185 190
 Ser Met Gly Ile Glu Ile Asn Ile Asp Pro Asn Ser Tyr Leu Lys Leu
 195 200 205
 Tyr Tyr Val Ile Val Ala Asp Arg Asn Leu Glu Gly Leu Arg Gln Lys
 210 215 220
 Ile Arg Lys Ile Asn Phe Ala Asn Val Glu Thr Ser Phe Thr Leu Thr
 225 230 235 240
 Tyr Met Phe Trp Arg Asn Trp Leu Lys Lys Asn Lys Leu Phe Arg Asn
 245 250 255
 Asn Leu Met Gln Asp Ile Lys Arg Val Tyr Asp Val Ser Leu Phe Val
 260 265 270
 Ile Arg Asn His Met Asp Val Asn Gly Ser Ile Ile Ala Ser Ser Asp
 275 280 285
 Phe Ser Phe Val Lys Ile Tyr Gly Asp Ser Tyr Gln Tyr Cys Trp Pro

290	295	300
Arg Asp Ala Ala Ile Ala Ala Tyr Ala Leu Asp Leu Ala Gly Tyr Lys		
305	310	315
Glu Leu Ala Leu Lys His Phe Gln Phe Ile Ser Asn Ile Ala Asn Ser		
325	330	335
Glu Gly Phe Leu Tyr His Lys Tyr Asn Pro Asn Thr Thr Leu Ala Ser		
340	345	350
Ser Trp His Pro Trp Tyr Tyr Lys Gly Lys Arg Ile Tyr Pro Ile Gln		
355	360	365
Gly Asp Glu Thr Ala Leu Glu Val Trp Ala Ile Ala Ser His Tyr Glu		
370	375	380
Lys Tyr Glu Asp Ile Asp Glu Ile Leu Pro Leu Tyr Lys Lys Phe Val		
385	390	395
Lys Pro Ala Leu Lys Phe Met Met Ser Phe Met Glu Glu Gly Leu Pro		
405	410	415
Lys Pro Ser Phe Asp Leu Trp Glu Glu Arg Tyr Gly Ile His Ile Tyr		
420	425	430
Thr Val Ser Thr Val Tyr Gly Ala Leu Thr Lys Gly Ala Lys Leu Ala		
435	440	445
Tyr Asp Val Gly Asp Glu Ile Leu Ser Glu Asp Leu Ser Asp Thr Ser		
450	455	460
Gly Leu Leu Lys Gly Met Val Leu Lys Arg Met Thr Tyr Asn Gly Arg		
465	470	475
Phe Val Arg Arg Ile Asp Glu Glu Asn Asn Gln Asp Leu Thr Val Asp		
485	490	495
Ser Ser Leu Tyr Ala Pro Phe Phe Gly Leu Val Asn Ala Asn Asp		
500	505	510
Lys Ile Met Ile Asn Thr Ile Asn Glu Ile Glu Ser Arg Leu Thr Val		
515	520	525
Asn Gly Gly Ile Ile Arg Tyr Glu Asn Asp Met Tyr Gln Arg Arg Lys		
530	535	540
Lys Gln Pro Asn Pro Trp Ile Ile Thr Thr Leu Trp Leu Ser Glu Tyr		
545	550	555
Tyr Ala Thr Ile Asn Asp Lys Asn Lys Ala Asn Glu Tyr Ile Lys Trp		
565	570	575
Val Ile Asn Arg Ala Leu Pro Thr Gly Phe Leu Pro Glu Gln Val Asp		
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Pro Glu Thr Phe Glu Pro Thr Ser Val Thr Pro Leu Val Trp Ser His		
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ttctacitgt gtgtttccgt ggtatggcaat ttcaactgga tagacagaaaa tgcaatcaag 180

cacatggact actacgacca caccatggc tctgtcgta actacacgc taacggatt	240
gatttcgaga acaggagata ggttgacata tacaaggaca tccttattag gccccgttt	300
gctgaaaaca agaccggtaa ggtatgtaaac ctgaagatct tcctcacca gaatttctac	360
atatatggca atgacatagg ggataccgt gcctacttc ctgaataccg cgggtgtatc	420
cattataagg gagggagata ctitctcgca tccactctt atgagagcgg taattctgc	480
gatcaaatatg ccacaggggt taaggatgt ggtgagctga agggcacatg gaaggatgcc	540
gaggacaatg aattatcaat gaacccgggt gcaataggtt cggtggatt tgctataagg	600
cattccacga ctctgaaggc cggttcaaag ttacgcgtt attatttcat catagcggga	660
agaaacatca acgatataga gagcgaatat tcaaattgtt atgtccagta cctccaaaag	720
cttctgggaa gaacaacaaa ctactgggg ctctgggtt cgaagggtac tcccagcctg	780
gattcagaca caacagcgtt ttacccgaga tcgctctcg tgactaagag ccacgaaac	840
gatcttgggg ccatagccgc atcctgcgc acgcataatac tgaagcttag ccatgacggg	900
tactactacg tctggcccg ggtgcctcc atggctgcat acgcctttag catabccggg	960
cacagcgaaa ccgcacgacg ctctttgc ctgtatggaa attcacttc agaaggaggaa	1020
tacctgtacc acaaatacaa cgtgcacggc aagatgcaca gcagctgggtt accgcacgtc	1080
atgaatggca aatccatata tccaatacag gaggatgaaa cagctctgtt ggtctggca	1140
ctctggaaat acttttagaa gtacaatgtt atcggcttca ccgcaccgtt ttatgaaacgc	1200
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Glu Asn His Ser Ser Gly His Pro Phe Tyr Phe Gly Val Ser Val Asp

35 40 45

Gly Asn Phe Asn Trp Ile Asp Arg Asn Ala Ile Lys His Met Asp Tyr

50 55 60

Tyr Asp His Thr Met Val Ser Val Val Asn Tyr Thr His Asn Gly Ile

65 70 75 80

Asp Phe Glu Asn Arg Asp Met Val Asp Ile Tyr Lys Asp Ile Phe Ile

85 90 95

Arg Arg Val Val Ala Glu Asn Lys Thr Gly Lys Asp Val Asn Leu Lys

100 105 110

115 120 125
 Thr Ala Ala Tyr Phe Pro Glu Tyr Arg Gly Val Ile His Tyr Lys Gly
 130 135 140
 Gly Arg Tyr Phe Leu Ala Ser Thr Leu Asp Glu Ser Gly Asn Phe Cys
 145 150 155 160
 Asp Gln Tyr Ala Thr Gly Val Lys Asp Val Gly Glu Leu Lys Gly Thr
 165 170 175
 Thr Ile Asp Ala Glu Asp Asn Glu Leu Ser Met Asn Pro Val Ala Ile
 180 185 190
 Ser Val Asp Ser Val Ile Arg His Ser Thr Thr Leu Lys Ala Gly
 195 200 205
 Ser Iys Phe Thr Leu Tyr Tyr Phe Ile Ile Ala Gly Arg Asn Ile Asn
 210 215 220
 Asp Glu Ser Glu Tyr Ser Asn Val Asn Val Gln Tyr Leu Gln Lys
 230 235 240
 Leu Arg Arg Thr Thr Asn Tyr Trp Glu Leu Trp Ser Ser Lys Val
 245 250 255
 Thr Pro Ser Leu Asp Ser Asp Thr Thr Ala Leu Tyr Arg Arg Ser Leu
 260 265 270
 Phe Val Thr Lys Ser His Ala Asn Asp Leu Gly Ala Ile Ala Ala Ser
 275 280 285
 Cys Asp Ser Asp Ile Leu Lys Leu Ser His Asp Gly Tyr Tyr Val
 290 295 300
 Trp Pro Arg Asp Ala Ser Met Ala Ala Tyr Ala Leu Ser Ile Ser Gly
 305 310 315 320
 His Ser Glu Thr Ala Arg Arg Phe Phe Ala Leu Met Glu Asp Ser Leu
 325 330 335
 Ser Glu Glu Gly Tyr Leu Tyr His Lys Tyr Asn Val Asp Gly Lys Ile
 340 345 350
 Ala Ser Ser Trp Leu Pro His Val Met Asn Gly Lys Ser Ile Tyr Pro
 355 360 365
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 370 375 380
 Phe Arg Lys Tyr Asn Asp Ile Gly Phe Thr Ala Pro Tyr Tyr Glu Arg
 385 390 395 400
 Leu Ile Thr Arg Ala Ala Asp Phe Met Thr Asn Phe Val Asp Asn Asn
 405 410 415
 Gly Leu Pro Lys Pro Ser Phe Asp Leu Trp Glu Glu Arg Tyr Gly Ile
 420 425 430
 His Ala Tyr Thr Val Ala Thr Val Tyr Ala Ala Leu Lys Ala Ala Ser
 435 440 445
 Asn Phe Ala Asn Val Phe Gly Asp Pro Asp Leu Ser Glu Lys Tyr Glu
 450 455 460
 Asn Ala Ala Glu Arg Met Tyr His Ala Phe Asp Glu Arg Phe Tyr Ser
 465 470 475 480
 Glu Asp Thr Gly Tyr Tyr Ala Arg Ala Ile Ile Asp Gly Lys Pro Asp
 485 490 495
 Phe Thr Val Asp Ser Ala Leu Thr Ser Leu Val Leu Phe Gly Met Lys
 500 505 510
 Asp Ala Asp Asp Pro Lys Val Ile Ser Thr Met Gln Arg Ile Ser Glu
 515 520 525

Asp Leu Trp Val Asn Gly Val Gly Gly Ile Ala Arg Tyr Gln Asn Asp
 530 535 540
 Arg Tyr Met Arg Val Lys Asp Asp Pro Ser Val Pro Gly Asn Pro Trp
 545 550 555 560
 Ile Ile Thr Thr Leu Trp Met Ala Arg Tyr Tyr Met Arg Phe Gly Asp
 565 570 575
 Phe Glu Lys Ala Trp Asn Leu Ile Gln Trp Val Lys Ser His Arg Gln
 580 585 590
 Lys Ser Gly Ile Phe Ser Glu Gln Ile Asn Pro Tyr Asn Gly Glu Pro
 595 600 605
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 610 615 620
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 625 630 635

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<212> DNA
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35 40 45
Val Lys Trp His Trp Asp Asp Asp Trp Asp Ile Ser Gln Lys Tyr Ile
50 55 60
Glu Glu Thr Asn Ile Phe Lys Thr Ile Leu Glu Asp Asp Lys Ile Ile
65 70 75 80
Leu Thr Ile Lys Asp Phe Val Pro Val Ser His Asn Val Ile Ile Arg
85 90 95
Arg Leu His Ile Lys Asn Lys Leu Asp Lys Lys Leu Asn Phe Lys Leu
100 105 110
Phe Phe Tyr Glu Asn Leu Arg Ile Gly Glu Tyr Pro Thr Glu Asn Ala
115 120 125
Val Arg Phe Leu Glu Asp Glu Gly Cys Ile Val Lys Tyr Asn Glu Lys
130 135 140
Tyr Val Phe Cys Ile Gly Ser Asn Lys Lys Ile Asp Ser Phe Gln Cys
145 150 155 160
Gly Asn Arg Tyr Ser Lys Asn Ser Ala Tyr Val Asp Ile Glu Asn Gly
165 170 175
Leu Leu Met Glu His Lys Glu Ser His Gly Leu Met Thr Asp Ser Ala
180 185 190
Ile Ser Trp Asn Ile Glu Ile Asp Lys Gly Lys Ser Leu Ala Phe Asn
195 200 205
Ile Tyr Ile Leu Leu Gln Lys Phe Asp Gly Asp Leu Ser Ile Ile Thr
210 215 220
Glu Gln Leu Lys Ile Ile Met Asn Asn Thr Val His Ile Lys Asp Leu
225 230 235 240
Ser Met Asn Tyr Trp Lys Asn Ser Ile Gly Asn Ile Lys Glu His Ile
245 250 255
His Pro Gln Phe His Ser Asp Lys Glu Ile Cys Pro Ile Ala Lys Arg
260 265 270
Ala Leu Met Val Leu Leu Met Leu Cys Asp Lys Asp Gly Gly Ile Ile
275 280 285
Ala Ala Pro Ser Leu His Pro Asp Tyr Arg Tyr Val Trp Gly Arg Asp
290 295 300
Gly Ala Tyr Ile Ala Ile Ala Leu Asp Leu Phe Gly Ile Arg Gly Ile
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Pro Asp Arg Phe Phe Glu Phe Met Ser Lys Ile Gln Asn Asp Asp Gly
325 330 335
Ser Trp Leu Gln Asn Tyr Tyr Asn Gly Lys Pro Arg Leu Thr Ala

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Tyr Arg Leu Thr Gly Asn Arg Lys Phe Val Glu Arg Tyr Trp Asn Thr		
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Ile Glu Lys Ala Gly Asn Tyr Leu Thr Ser Ala Ala Leu Asn Phe Thr		
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395	400	
Pro Cys Phe Asp Leu Trp Glu Glu Lys Phe Gly Val Phe Ala Tyr Thr		
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Met Gly Ala Ile Tyr Ala Gly Leu Lys Ala Ala Tyr Ser Met Ser Lys		
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Ala Val Asp Met Arg Asp Lys Val Lys His Trp Glu Lys Ala Ile Glu		
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Phe Leu Lys Lys Glu Val Pro Arg Arg Phe Tyr Leu Glu Asp Glu Glu		
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Arg Phe Ala Lys Ser Ile Asn Pro Leu Asp Lys Glu Ile Asp Ala Ser		
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475	480	
Ile Leu Gly Leu Ser Tyr Pro Phe Asn Leu Ile Asp Val Asp Asp Glu		
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Arg Met Ile Lys Thr Ala Glu Ala Ile Glu Asn Ala Phe Asn Tyr Lys		
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Val Gly Gly Ile Gly Arg Tyr Pro Asn Asp Val Tyr Phe Gly Gly Asn		
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Ser Lys Val Leu Lys Glu Lys Asn Lys Asn Asp Met Ala Glu Lys Tyr		
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555	560	
Leu Lys Lys Ser Lys Lys Leu Phe Asp Trp Ala Val Lys Tyr Ser Phe		
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Asn Gly Leu Phe Pro Glu Gln Ile His Lys Asp Leu Gly Ile Pro Met		
580	585	590
Ser Ala Met Pro Leu Gly Trp Ser Asn Ala Met Phe Leu Ile Tyr Leu		
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Tyr Lys Asp Asp Asn Val Ile Ile Pro		
610	615	

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<211> 1866

<212> DNA

<213> Archaea

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tatctcaaag attccaacat attaaaaaca acttatgaaa atgatgactt ctaatataat	240
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aagaccaatt cagaaaagga cataaaaatta tttttttagt aaaatttgag aataggtgaa	360
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aaaaattata tttctgtat tggcagtaat aaaaaagtat cctcttacca atgtgggatt	480
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 caaaaataca ctcttcaat actcatactt cctgaaaagt atgatggtga ttataataaa 660
 accctaaact taatggatac tctacacatg gtaaaagaca acctcaaaga cctatataac 720
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<211> 621

<212> PRT

<213> Archaea

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 35 40 45
 Trp His Trp Asp His Ser Trp Asp Val Ser Gln Asn Tyr Leu Lys Asp
 50 55 60
 Ser Asn Ile Leu Lys Thr Thr Tyr Glu Asn Asp Asp Phe Leu Ile Tyr
 65 70 75 80
 Ser Lys Asp Cys Val Ser Ile Ser His Asn Leu Ile Val Lys Gln Leu
 85 90 95
 Ser Ile Ile Asn Lys Thr Asn Ser Glu Lys Asp Ile Lys Leu Phe Phe
 100 105 110
 Tyr Glu Asn Leu Arg Ile Gly Glu Thr Pro Ser Lys Ser Thr Val Lys
 115 120 125
 Phe Val Lys Glu Lys Asn Cys Leu Ile Lys His Asp Lys Asn Tyr Ile
 130 135 140
 Phe Cys Ile Gly Ser Asn Lys Lys Val Ser Ser Tyr Gln Cys Gly Ile
 145 150 155 160
 Lys Tyr Ser Glu Ser Ser Ala Leu Arg Asp Ile Glu Asn Gly Val Leu

165 170 175
 Lys Glu Gln Ser Ser Ala Thr Gly Leu Ile Thr Asp Ser Ala Leu Cys
 180 185 190
 Trp Glu Phe Lys Ile Lys Pro Asn Gln Lys Tyr Thr Leu Ser Ile Leu
 195 200 205
 Ile Leu Pro Glu Lys Tyr Asp Gly Asp Tyr Asn Lys Thr Leu Asn Leu
 210 215 220
 Met Asp Thr Leu His Met Val Lys Asp Asn Leu Lys Asp Leu Tyr Asn
 225 230 235 240
 Leu Thr Arg Asn Phe Trp Lys Ser Arg Val Asp Ser Met Val Asn Lys
 245 250 255
 Trp Gly Ile Leu Lys Leu Glu Glu Tyr Lys Glu Cys Ile Asp Ile Cys
 260 265 270
 Lys Arg Ser Leu Leu Thr Leu Leu Leu Cys Asp Tyr Lys Gly Gly
 275 280 285
 Ile Ile Ala Ser Pro Ser Leu His Pro Asp Tyr Arg Tyr Val Trp Cys
 290 295 300
 Arg Asp Ala Gly Tyr Met Ala Val Ala Leu Asp Leu Cys Gly Gln His
 305 310 315 320
 Glu Met Ser Glu Lys Tyr Phe Glu Trp Cys Lys Thr Thr Gln Asn Ser
 325 330 335
 Asp Gly Ser Trp Val Gln Asn Tyr Tyr Val Glu Gly Tyr Pro Arg Phe
 340 345 350
 Thr Ala Ile Gln Ile Asp Gln Val Gly Thr Thr Ile Trp Ala Leu Leu
 355 360 365
 Val His Tyr Arg Ile Thr Gly Asp Lys His Phe Leu Lys Arg Asn Trp
 370 375 380
 Glu Met Val Lys Ala Gly Asp Tyr Leu Ser Arg Ala Ala Asp Gln
 385 390 395 400
 Leu Ile Pro Cys Tyr Asp Leu Trp Glu Glu Lys Phe Gly Val Phe Ala
 405 410 415
 Tyr Thr Leu Gly Ala Ile Tyr Gly Leu Lys Ser Gly Tyr Leu Ile
 420 425 430
 Gly Lys Glu Leu Asp Lys Glu Glu Ile Gln His Trp Lys Lys Ser
 435 440 445
 Met Asn Phe Leu Lys Asn Glu Val Val Asn Arg Leu Tyr Leu Lys Asn
 450 455 460
 Glu Lys Arg Phe Ala Lys Ser Leu Lys Pro Leu Asp Lys Thr Ile Asp
 465 470 475 480
 Thr Ser Ile Leu Gly Leu Ser Phe Pro Tyr Gly Leu Val Ser Val Asp
 485 490 495
 Asp Pro Arg Ile Ile Ser Thr Ala Asn Gln Ile Glu Lys Ala Phe Asn
 500 505 510
 Tyr Lys Val Gly Gly Val Gly Arg Tyr Pro Glu Asp Ile Tyr Phe Gly
 515 520 525
 Gly Asn Pro Trp Ile Ile Thr Thr Leu Trp Leu Tyr Met Tyr Tyr Lys
 530 535 540
 Lys Leu Val Asp Thr Leu Ser Lys Lys Gly Lys Phe Gln Glu Ser Ile
 545 550 555 560
 Ile Asp Asn Tyr Asn Lys Lys Cys Tyr Asn Leu Leu Lys Trp Ile Leu
 565 570 575

Lys His Gln Phe Asn Gly Met Phe Pro Glu Gln Val His Lys Asp Leu
 580 585 590
 Gly Ile Pro Ile Ser Ala Ile Pro Leu Gly Trp Ser His Ala Met Val
 595 600 605
 Ile Ile Ala Ile His Gly Asp Tyr Asp Ile Leu Ile Pro
 610 615 620

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 > DNA
 > Archaea

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 Val Lys Trp His Trp Asp Asp Asp Trp Asp Ile Thr Gln Lys Tyr Ile
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 Glu Glu Thr Asn Ile Phe Lys Thr Ile Leu Glu Asp Asp Lys Ile Ile
 65 70 75 80
 Leu Thr Ile Lys Asp Phe Val Pro Val Ser His Asn Val Leu Ile Arg
 85 90 95
 Arg Val Tyr Ile Lys Asn Lys Leu Asp Lys Lys Leu Asn Phe Lys Leu
 100 105 110
 Phe Phe Tyr Glu Asn Leu Arg Ile Gly Glu Asn Pro Ile Thr Asn Thr
 115 120 125
 Val Lys Phe Leu Glu Asp Gly Cys Ile Val Lys Tyr Asn Gly Lys Tyr
 130 135 140
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 145 150 155 160
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 165 170 175
 Leu Lys Glu His Lys Glu Ser Ser Gly Leu Leu Thr Asp Ser Ala Ile
 180 185 190
 Ser Trp Asn Ile Lys Ile Asp Glu Lys Arg Ser Leu Ala Phe Asn Ile
 195 200 205
 Tyr Ile Leu Pro Gln Arg Phe Asp Gly Asp Phe Ser Ile Ile Thr Glu
 210 215 220
 Gln Leu Lys Ile Ile Met Asn Asn Ser Glu Asn Ile Lys Asn Leu Ser
 225 230 235 240
 Met Asn Tyr Trp Lys His Ile Ile Gly Glu Ile Asn Arg Phe Ile His
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 Pro Glu Leu Arg Gln Asn Asn Lys Ile Tyr Ser Ile Thr Lys Arg Ala
 260 265 270
 Leu Met Thr Leu Leu Met Leu Cys Asp Lys Glu Gly Gly Ile Ile Ala
 275 280 285
 Ala Pro Ser Leu His Pro Asp Tyr Arg Tyr Val Trp Gly Arg Asp Gly
 290 295 300
 Ser Tyr Ile Ser Ile Ala Leu Asp Leu Phe Gly Ile Arg Asn Ile Pro
 305 310 315 320
 Asp Arg Phe Phe Glu Phe Met Ser Lys Ile Gln Asn Ala Asp Gly Ser
 325 330 335
 Trp Leu Gln Asn Tyr Tyr Val Asn Gly Lys Pro Arg Leu Thr Ala Ile
 340 345 350
 Gln Thr Asp Gln Ile Gly Ser Ile Leu Trp Ala Met Asp Val His Tyr
 355 360 365
 Arg Leu Thr Gly Asp Arg Lys Phe Val Glu Arg Tyr Trp Asn Thr Ile
 370 375 380
 Glu Lys Ala Ala Asn Tyr Leu Arg Leu Val Ala Leu Asn Phe Thr Pro
 385 390 395 400
 Cys Phe Asp Leu Trp Glu Glu Arg Phe Gly Val Phe Ala Tyr Thr Met

Gly Ala Thr Tyr Ala Gly Leu Lys Cys Ala Tyr Ser Met Ser Lys Ala
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 Val Asn Lys Arg Asp Lys Val Lys Asp Trp Gly Lys Thr Ile Glu Phe
 420 425 430
 435 440 445
 Leu Lys His Glu Val Pro Lys Arg Phe Tyr Leu Glu Asp Glu Glu Arg
 450 455 460
 Phe Ala Lys Ser Ile Asn Pro Leu Asp Lys Thr Ile Asp Thr Ser Ile
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 Leu Gly Leu Ser Tyr Pro Phe Asn Leu Ile Asp Val Asp Asp Glu Arg
 485 490 495
 Met Ile Lys Thr Ala Glu Ala Ile Glu Lys Ala Phe Lys Tyr Lys Val
 500 505 510
 Gly Gly Ile Gly Arg Tyr Pro Glu Asp Ile Tyr Phe Gly Gly Asn Pro
 515 520 525
 Trp Ile Ile Thr Thr Leu Trp Leu Ser Leu Tyr Tyr Arg Arg Leu Tyr
 530 535 540
 Lys Val Leu Lys Glu Lys Asp Asp Asn Gly Ala Asp Ile Tyr Leu Gln
 545 550 555 560
 Lys Ser Lys Lys Leu Phe Asn Trp Val Met Lys Tyr Ser Phe Asp Gly
 565 570 575
 Leu Phe Pro Glu Gln Ile His Lys Glu Leu Gly Val Pro Met Ser Ala
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 Asn Asp Lys Val Ile Ile Pro
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<212> DNA
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aatcagaact atttaaaaga tacaaacata ttggaaaacat catafgaaaa cgaggatttt	240
ctaataaatgaaat caaaggacta cgtgc当地 tcccataact cgataattaa gcaaataatca	300
atataaaaca aatccagcga aaaaaagaat taaaactgt tttttgc当地 aaatttaaga	360
atgggagaaaa ttccctgaagt aagtactgta aagtatagaa agaacagggatgtcattt	420
aaatacgata agaattatgt ttgttgc当地 ggcagtaata aaaaagtatc ttcataccaa	480
tgtgtgttgc当地 ggtcatccga gagtagtgcc ctaaatgatc taaaaatgg tattttaaag	540
gaatacgata gtgctgaagg cctaattcaca gatagcgc当地 tgggtgggatcccttgatgt	600
agtccaaatc aggaacagaa agtctcaata ttatatttg cagataagta tggggat	660
tataccaaaa ttatgttgc当地 attggataca ctaaatatag ttataaccatc acgc当地	720
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aattttaaaaa gaataaaaaca gatgttgc当地 atttgtaaaaa gatcccttatttca aaccattttca	900
ctcccttgc当地 atcataatgg tggataatttgc当地 cactc当地 tccatcc agatattatgat	960
tatgtatgttgc当地 gtggggacgc aggttataf gccgtcgc当地 ttgacctatg tggcagcat	1020

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 aacagatatt gggaaatgt taaaaaagca ggggattatt taagtagtgt tgccaatcca 1260
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<211> 677

<212> PRT

<213> Archaea

<400> 12

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 35 40 45
 Lys Leu Lys Trp Asn Trp Asp Asn Ser Trp Asp Ile Asn Gln Asn Tyr
 50 55 60
 Leu Lys Asp Thr Asn Ile Leu Lys Thr Ser Tyr Glu Asn Glu Asp Phe
 65 70 75 80
 Leu Ile Glu Ser Lys Asp Tyr Val Pro Ile Ser His Asn Ser Ile Ile
 85 90 95
 Lys Gln Ile Ser Ile Leu Asn Lys Ser Ser Glu Lys Lys Asn Leu Lys
 100 105 110
 Leu Phe Phe Tyr Glu Asn Leu Arg Met Gly Glu Ile Pro Glu Val Ser
 115 120 125
 Thr Val Lys Tyr Arg Lys Asn Arg Glu Cys Ile Ile Lys Tyr Asp Lys
 130 135 140
 Asn Tyr Val Phe Cys Ile Gly Ser Asn Lys Lys Val Ser Ser Tyr Gln
 145 150 155 160
 Cys Gly Val Arg Ser Ser Glu Ser Ser Ala Leu Asn Asp Leu Lys Asn
 165 170 175
 Gly Ile Leu Lys Glu Tyr Asp Ser Ala Glu Gly Leu Ile Thr Asp Ser
 180 185 190
 Ala Leu Gly Trp Asp Leu Glu Leu Ser Pro Asn Gln Glu Gln Lys Val
 195 200 205
 Ser Ile Phe Ile Phe Ala Asp Lys Tyr Gly Gly Asp Tyr Thr Lys Ile

210 215 220
 Met Asn Leu Leu Asp Thr Leu Asn Ile Val Ile Thr Asn His Ala Asp
 225 230 235 240
 Ile Tyr Asp Leu Thr Met Ala Tyr Trp Lys Asn Met Ile Glu Thr Thr
 245 250 255
 Ala Asn Ser Leu Cys Asn Ser Asn Gln Val Phe Lys Asp Leu Thr His
 260 265 270
 Ile Lys Asp Asp Ala Asn Ile Ser Asn Leu Lys Arg Ile Lys Gln Tyr
 275 280 285
 Glu Ala Ile Cys Lys Arg Ser Leu Leu Thr Ile Leu Leu Cys Asp
 290 295 300
 His Asn Gly Gly Ile Ile Ala Ser Pro Ser Leu Tyr Pro Asp Tyr Arg
 305 310 315 320
 Tyr Val Trp Cys Arg Asp Ala Gly Tyr Met Ala Val Ala Leu Asp Leu
 325 330 335
 Cys Gly Gln His Gly Ile Ser Glu Lys Tyr Phe Glu Trp Cys Lys Lys
 340 345 350
 Thr Gln Asn Ser Asp Gly Ser Trp Val Gln Asn Tyr Tyr Val Glu Gly
 355 360 365
 Asn Pro Arg Leu Thr Ala Ile Gln Ile Asp Gln Val Gly Thr Thr Ile
 370 375 380
 Trp Ala Ala Leu Val His Tyr Arg Ile Thr Arg Asp Lys Leu Phe Leu
 385 390 395 400
 Asn Arg Tyr Trp Glu Met Ile Lys Lys Ala Gly Asp Tyr Leu Ser Ser
 405 410 415
 Val Ala Asn Pro Pro Ser Pro Ser Tyr Asp Leu Trp Glu Glu Lys Tyr
 420 425 430
 Gly Val Phe Ala Tyr Thr Leu Gly Ala Ile Tyr Gly Gly Leu Lys Ser
 435 440 445
 Ala Tyr Asn Ile Cys Lys Ile Leu Gly Lys Glu Glu His Asp Ile Gln
 450 455 460
 Asn Trp Lys Glu Ser Met Asp Phe Leu Lys Asn Glu Met Val Asp Arg
 465 470 475 480
 Leu Tyr Leu Lys Asp Glu Asn Arg Phe Ala Lys Ser Leu Asp Pro Leu
 485 490 495
 Asp Lys Ala Leu Asp Ala Ser Ile Leu Gly Leu Ser Phe Pro Tyr Asn
 500 505 510
 Leu Val Pro Val Asp Asp Pro Arg Met Ile Ser Thr Ala Asn Gln Ile
 515 520 525
 Glu Asn Ala Phe Lys Tyr Lys Val Gly Gly Ile Gly Arg Tyr Pro Glu
 530 535 540
 Asp Val Tyr Phe Gly Gly Asn Pro Trp Ile Ile Thr Thr Ile Trp Leu
 545 550 555 560
 His Met Tyr Tyr Glu Asn Leu Ile Lys Ser Leu Ser Lys His Gly Lys
 565 570 575
 Asn Ala Ile His Ser Asp Gln Ile Pro Asp Ser Ser Gly Asp Leu Lys
 580 585 590
 Asp Phe Val Ser Ile Ile Gly Ser Ile Glu Asn His Gly Glu Lys Ser
 595 600 605
 Asp Glu Thr Pro Ser Ser Asp Thr Leu Leu Thr Tyr Ala Gln Lys Cys
 610 615 620

Asn Asn Leu Phe Asp Trp Thr Leu Lys Tyr Asn Phe Asn Glu Leu Phe
 625 630 635 640
 Pro Glu Gln Val His Lys Asp Leu Gly Ala Pro Ile Ser Ala Ile Pro
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 ttatgtccca ttacacataa tgtttaattt aggagagttt tcattaaaaaa taaacttcca 300
 tataattata attttaaaact attttctat gaaaatcta gaattggaga acatccctca 360
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<212> PRT

<213> Unknown

<220>

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35 40 45
Ile Lys Glu Trp Ser Val Tyr Gln Lys Tyr Ile Glu Asp Thr Asn Ile
55 60
Ile Lys Thr Thr Leu Glu Asn Glu Asn Ile Ile Phe Val Ile Lys Asp
70 75 80
Leu Val Pro Ile Ser His Asn Val Leu Ile Arg Arg Val Phe Ile Lys
85 90 95
Asn Lys Leu Pro Tyr Asn Tyr Asn Phe Lys Leu Phe Phe Tyr Glu Asn
100 105 110
Leu Arg Ile Gly Glu His Pro Ser Glu Asn Thr Val Lys Phe Leu Asp
115 120 125
Asp Cys Ile Val Lys Phe Asn Gly Lys Tyr Thr Phe Cys Ile Ser Ser
130 135 140
Asp Lys Lys Ile Asn Ser Tyr Gln Cys Gly Asn Arg Tyr Ser Glu Lys
145 150 155 160
Ser Ala Tyr Lys Asp Ile Glu Asn Gly Leu Leu Ser Glu Asn Pro Glu
165 170 175
Ser Val Gly Val Leu Thr Asp Ser Ala Ile Glu Trp Asp Ile Asp Leu
180 185 190
Lys Pro His Gly Lys Val Ala Phe Asn Ile Tyr Ile Phe Pro His Ile
195 200 205
Gly Asn Asn Ile Glu Ile Ile Lys Asn Gln Leu Asn Ile Ile Lys Asn
210 215 220
Leu Ser Ser Glu Ile Lys Asn Ile Ser Leu Asn Tyr Trp Lys Ser Ser
225 230 235 240
Phe Asp Ile Lys Gly Tyr Leu Phe Asn Glu Lys Tyr Leu Lys Leu Ala
245 250 255
Lys Arg Ala Leu Met Ile Leu Thr Met Leu Ser Asp Lys Asn Gly Gly
260 265 270
Ile Ile Ala Ser Pro Ser Ile His Pro Asp Tyr Arg Tyr Val Trp Gly
275 280 285
Arg Asp Gly Ser Tyr Met Ala Val Ala Leu Ser Ile Tyr Gly Ile Lys
290 295 300
Asn Ile Pro Trp Arg Phe Phe His Phe Met Ser Lys Val Gln Asn Leu
305 310 315 320
Asp Gly Ser Trp Leu Gln Asn Tyr Tyr Thr Asp Gly Lys Pro Arg Leu
325 330 335
Thr Ala Leu Gln Ile Asp Gln Ile Gly Ser Val Leu Trp Ala Met Glu
340 345 350

Val Tyr Tyr Arg Thr Thr Gly Asp Arg Glu Phe Val Lys Lys Phe Trp
 355 360 365
 Glu Thr Ile Glu Lys Ala Gly Asn Phe Leu Tyr Asn Ala Ser Leu Ser
 370 375 380
 Leu Met Pro Cys Phe Asp Leu Trp Glu Glu Lys Tyr Gly Val Phe Ser
 385 390 395 400
 Tyr Thr Leu Gly Ala Met Tyr Gly Gly Leu Arg Ala Gly Cys Ser Leu
 405 410 415
 Ala Lys Ala Ile Glu Glu Lys Lys Glu Asp Trp Lys Lys Ala Leu Asp
 420 425 430
 Lys Leu Lys Lys Asp Val Asp Leu Leu Tyr Leu Ser Asp Glu Glu Arg
 435 440 445
 Phe Val Lys Ser Ile Asn Pro Leu Asn Lys Glu Ile Asp Thr Ser Ile
 450 455 460
 Leu Gly Leu Ser Tyr Pro Phe Gly Leu Val Lys Val Asn Asp Glu Arg
 465 470 475 480
 Met Ile Lys Thr Ala Glu Ala Ile Glu Lys Ala Phe Lys Tyr Lys Val
 485 490 495
 Gly Gly Ile Gly Arg Tyr Pro Ser Asp Val Tyr Phe Gly Gly Asn Pro
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 515 520 525
 Ile Thr Thr Asn Asp Arg Lys Tyr Leu Glu Lys Ser Lys Lys Leu Phe
 530 535 540
 Asn Trp Val Ile Asn His Ile Tyr Leu Phe Pro Glu Gln Ile His Lys
 545 550 555 560
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<210> 15

<211> 2121

<212> DNA

<213> Bacterial

<400> 15

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gggactgcaa acaactatac ttccaaagta tggtttacca ttgcagacgg ggggatatct 240
gaggtttact atccgactat agatactgtc gatgtaaagg atattaaatt ttttgtgaca 300
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gctgaaagag atggaaatttta cactgcattg tcattgtaca taggatggaa aaagtattcg 660
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tacaattacg acagtgtcaag agggaaatc atagaagggtg ctgagataga tcattaaagaaa 780
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 Ala Asn Gly Asn Val Ala Leu Ile Ala Glu Arg Asp Gly Ile Tyr Thr
 195 200 205
 Ala Leu Ser Ser Asp Ile Gly Trp Lys Lys Tyr Ser Ile Gly Tyr Tyr
 210 215 220
 Lys Val Asn Asp Ile Glu Thr Asp Leu Tyr Lys Asn Met Gln Met Thr
 225 230 235 240
 Tyr Asn Tyr Asp Ser Ala Arg Gly Asn Ile Ile Glu Gly Ala Glu Ile
 245 250 255
 Asp Leu Lys Lys Asn Arg Gln Phe Glu Ile Val Leu Ser Phe Gly Gln
 260 265 270
 Ser Glu Asp Glu Ala Val Lys Thr Asn Met Glu Thr Leu Asn Asp Asn
 275 280 285
 Tyr Asp Ser Leu Lys Ala Tyr Ile Asp Gln Trp Glu Lys Tyr Cys
 290 295 300
 Asp Ser Leu Asn Asp Phe Gly Gly Lys Ala Asn Ser Leu Tyr Phe Asn
 305 310 315 320
 Ser Met Met Ile Leu Lys Ala Ser Glu Asp Lys Thr Asn Lys Gly Ala
 325 330 335
 Tyr Ile Ala Ser Leu Ser Ile Pro Trp Gly Asp Gly Gln Glu Asp Asp
 340 345 350
 Asn Ile Gly Gly Tyr His Leu Val Trp Ser Arg Asp Leu Tyr His Val
 355 360 365
 Ala Asn Ala Phe Ile Val Ala Gly Asp Thr Asp Ser Ala Asn Arg Ala
 370 375 380
 Leu Asp Tyr Leu Asp Lys Val Val Lys Asp Asn Gly Met Ile Pro Gln
 385 390 395 400
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 Glu Gln Ala Asp Pro Ile Ile Leu Ser Tyr Arg Leu Lys Arg Tyr Asp
 420 425 430
 Leu Tyr Glu Ser Leu Val Lys Pro Leu Ala Asp Phe Ile Met Lys Ile
 435 440 445
 Gly Pro Lys Thr Gly Gln Glu Arg Trp Glu Glu Ile Gly Gly Tyr Ser
 450 455 460
 Pro Ala Thr Leu Ala Ser Glu Val Ala Gly Leu Thr Cys Ala Ala Tyr
 465 470 475 480
 Ile Ala Glu Gln Asn Lys Asp Phe Glu Ser Ala Lys Lys Tyr Gln Glu
 485 490 495
 Lys Ala Asp Asn Trp Gln Arg Leu Ile Asp Asn Leu Thr Tyr Thr Glu
 500 505 510
 Lys Gly Pro Leu Gly Asp Gly His Tyr Tyr Ile Arg Ile Ala Gly Leu
 515 520 525
 Pro Asp Pro Asn Ala Asp Phe Met Ile Ser Ile Ala Asn Gly Gly Gly
 530 535 540
 Val Tyr Asp Gln Lys Glu Ile Val Asp Pro Ser Phe Leu Glu Leu Val
 545 550 555 560
 Arg Leu Gly Val Lys Ser Ala Asp Asp Pro Lys Ile Leu Asn Thr Leu
 565 570 575
 Lys Val Val Asp Glu Thr Ile Lys Val Asp Thr Pro Lys Gly Pro Ser

580 585 590
Trp Tyr Arg Tyr Asn His Asp Gly Tyr Gly Glu Met Ser Lys Thr Glu
595 600 605
Leu Tyr His Gly Thr Gly Lys Gly Arg Leu Trp Pro Leu Leu Thr Gly
610 615 620
Glu Arg Gly Met Tyr Glu Ile Ala Ala Glu Tyr Asp Asp Val Ile Ile
625 630 635 640
Ile Lys Thr Arg Ile Gly Leu Leu Lys Gly Ser Arg Ile Arg Phe Glu
645 650 655
Tyr Asp Ile Val Lys Glu Asp Glu Asn Lys Leu Leu Ala Gln Gly Met
660 665 670
Thr Glu His Pro Phe Thr Thr Leu Asp Arg Lys Pro Val Asn Ile Lys
675 680 685
Lys Ile Leu Pro His Val Tyr Glu Met Leu Asn Lys Cys Tyr Asp Asp
690 695 700
Gly Val
705

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